

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: CORUZZI, GLORIA
LAM, HON-MING
HSIEH, MING-HSIUN
- (ii) TITLE OF THE INVENTION: PLANT NITROGEN REGULATORY
P-PII GENES
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: PENNIE & EDMONDS LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/899,330
(B) FILING DATE: 23-JUL-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/022,328
(B) FILING DATE: 24-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Coruzzi, Laura A
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 5914-042-999
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe	Tyr	Lys	Val	Glu	Ala	Ile	Val	Arg	Pro	Trp	Arg	Ile	Gln	Gln	Val
1				5				10					15		
Ser	Ser	Ala	Leu	Leu	Lys	Ile	Gly	Ile	Arg	Gly	Val	Thr	Val	Ser	Asp
			20				25						30		

Val	Arg	Gly	Phe	Gly	Ala	Gln	Gly	Gly	Ser	Thr	Glu	Arg	His	Gly	Gly
		35					40					45			
Ser	Glu	Phe	Ser	Glu	Asp	Lys	Phe	Val	Ala	Lys	Val	Lys	Met	Glu	Ile
	50					55					60				
Val	Val	Lys	Lys	Asp	Gln	Val	Glu	Ser	Val	Ile	Asn	Thr	Ile	Ile	Glu
65					70					75					80
Gly	Ala	Arg	Thr	Gly	Glu	Ile	Gly	Asp	Gly	Lys	Ile	Phe	Val	Leu	Pro
				85					90					95	
Val	Ser	Asp	Val	Ile	Arg	Val	Arg	Thr	Gly	Glu	Arg	Gly	Glu	Lys	Ala
			100					105					110		
Glu															

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe	Tyr	Lys	Val	Glu	Ala	Ile	Leu	Arg	Pro	Trp	Arg	Val	Ser	Gln	Val
1				5					10					15	
Ser	Ser	Ala	Leu	Leu	Lys	Ile	Gly	Ile	Arg	Gly	Val	Thr	Val	Ser	Asp
		20						25				30			
Val	Arg	Gly	Phe	Gly	Ala	Gln	Gly	Gly	Ser	Thr	Glu	Arg	Gln	Gly	Gly
		35					40					45			
Ser	Glu	Phe	Ser	Glu	Asp	Lys	Phe	Val	Ala	Lys	Val	Lys	Met	Glu	Ile
	50					55					60				
Val	Val	Ser	Lys	Asp	Gln	Val	Glu	Asp	Val	Ile	Glu	Lys	Ile	Ile	Glu
65					70					75					80
Glu	Ala	Arg	Thr	Gly	Glu	Ile	Gly	Asp	Gly	Lys	Ile	Phe	Leu	Leu	Pro
				85					90					95	
Val	Ser	Asp	Val	Ile	Arg	Val	Arg	Thr	Gly	Glu	Arg	Gly	Asp	Lys	Ala
			100					105					110		
Glu															

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Lys	Lys	Ile	Asp	Ala	Ile	Ile	Lys	Pro	Phe	Lys	Leu	Asp	Asp	Val
1				5					10					15	
Arg	Glu	Ala	Leu	Ala	Glu	Val	Gly	Ile	Thr	Gly	Met	Thr	Val	Thr	Glu
			20					25					30		
Val	Lys	Gly	Phe	Gly	Arg	Gln	Lys	Gly	His	Thr	Glu	Leu	Tyr	Arg	Gly
		35					40					45			
Ala	Glu	Tyr	Met	Val	Asp	Phe	Leu	Pro	Lys	Val	Lys	Ile	Glu	Ile	Val
	50					55					60				
Val	Thr	Asp	Asp	Ile	Val	Asp	Thr	Cys	Val	Asp	Thr	Ile	Ile	Arg	Thr
65					70					75					80
Ala	Gln	Thr	Gly	Lys	Ile	Gly	Asp	Gly	Lys	Ile	Phe	Val	Phe	Asp	Val
				85					90					95	
Ala	Arg	Val	Ile	Arg	Ile	Arg	Thr	Gly	Glu	Glu	Asp	Asp	Ala	Ala	Ile

100

105

110

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Lys Lys Ile Asp Ala Ile Ile Lys Pro Phe Lys Leu Asp Asp Val
 1      5      10
Arg Glu Ala Leu Ala Glu Val Gly Ile Thr Gly Met Thr Val Thr Glu
 20      25      30
Val Lys Gly Phe Gly Arg Gln Lys Gly His Thr Glu Leu Tyr Arg Gly
 35      40      45
Ala Glu Tyr Met Val Asp Phe Leu Pro Lys Val Lys Ile Glu Ile Val
 50      55      60
Val Pro Asp Asp Ile Val Asp Thr Cys Val Asp Thr Ile Ile Arg Thr
 65      70      75      80
Ala Gln Thr Gly Lys Ile Gly Asp Gly Lys Ile Phe Val Phe Asp Val
 85      90      95
Ala Arg Val Ile Arg Ile Arg Thr Gly Glu Glu Asp Asp Ala Ala Ile
 100      105      110

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Lys Lys Ile Glu Ala Ile Ile Lys Pro Phe Lys Leu Asp Glu Val
 1      5      10      15
Arg Ser Pro Ser Gly Val Gly Leu Gln Gly Ile Thr Val Thr Glu Ala
 20      25      30
Lys Gly Phe Gly Arg Gln Lys Gly His Thr Glu Leu Tyr Arg Gly Ala
 35      40      45
Glu Tyr Val Val Asp Phe Leu Pro Lys Val Lys Val Glu Val Val Leu
 50      55      60
Ala Asp Glu Asn Ala Glu Ala Val Ile Glu Ala Ile Arg Lys Ala Ala
 65      70      75      80
Gln Thr Gly Arg Ile Gly Asp Gly Lys Ile Phe Val Ser Asn Val Glu
 85      90      95
Glu Val Ile Arg Ile Arg Thr Gly Glu Thr Gly Ile Asp Ala Ile
 100      105      110

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Lys	Lys	Ile	Glu	Ala	Ile	Ile	Lys	Pro	Phe	Lys	Leu	Asp	Glu	Val
1				5					10					15	
Arg	Ser	Leu	Ser	Gly	Val	Gly	Leu	Gln	Gly	Ile	Thr	Val	Thr	Glu	Ala
			20					25					30		
Lys	Gly	Phe	Gly	Arg	Gln	Lys	Gly	His	Thr	Asp	Leu	Tyr	Arg	Gly	Ala
		35					40					45			
Glu	Tyr	Ile	Val	Asp	Phe	Leu	Pro	Lys	Val	Lys	Ile	Glu	Ile	Val	Ile
	50					55					60				
Gly	Asp	Asp	Leu	Val	Glu	Arg	Ala	Ile	Asp	Ala	Ile	Arg	Arg	Ala	Ala
65					70					75					80
Gln	Thr	Gly	Arg	Ile	Gly	Asp	Gly	Lys	Ile	Phe	Val	Ser	Asn	Ile	Glu
				85					90					95	
Glu	Ala	Ile	Arg	Ile	Arg	Thr	Gly	Glu	Ser	Gly	Leu	Asp	Ala	Ile	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Lys	Lys	Ile	Glu	Ala	Ile	Ile	Lys	Pro	Phe	Lys	Leu	Asp	Glu	Val
1				5					10					15	
Lys	Glu	Ala	Leu	His	Glu	Val	Gly	Ile	Lys	Gly	Ile	Thr	Val	Thr	Glu
			20					25					30		
Ala	Lys	Gly	Phe	Gly	Arg	Gln	Lys	Gly	His	Thr	Glu	Leu	Tyr	Arg	Gly
		35					40					45			
Ala	Glu	Tyr	Val	Val	Asp	Phe	Leu	Pro	Lys	Val	Lys	Ile	Glu	Val	Val
	50					55					60				
Met	Glu	Asp	Ser	Leu	Val	Glu	Arg	Ala	Ile	Glu	Ala	Ile	Gln	Gln	Ala
65					70					75					80
Ala	His	Thr	Gly	Arg	Ile	Gly	Asp	Gly	Lys	Ile	Phe	Val	Thr	Pro	Val
				85					90					95	
Glu	Glu	Val	Val	Arg	Ile	Arg	Thr	Gly	Glu	Lys	Gly	Gly	Asp	Ala	Ile
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Lys	Lys	Val	Glu	Ala	Ile	Ile	Lys	Pro	Phe	Lys	Leu	Asp	Glu	Val
1				5					10					15	
Lys	Glu	Ala	Leu	Gln	Glu	Ala	Gly	Ile	Gln	Gly	Leu	Ser	Val	Ile	Glu
			20					25					30		
Val	Lys	Gly	Phe	Gly	Arg	Gln	Lys	Gly	His	Thr	Glu	Leu	Tyr	Arg	Gly
		35					40					45			
Ala	Glu	Tyr	Val	Val	Asp	Phe	Leu	Pro	Lys	Val	Lys	Ile	Glu	Met	Val
	50					55					60				
Leu	Pro	Asp	Glu	Met	Val	Asp	Ile	Ala	Ile	Glu	Ala	Ile	Val	Gly	Ala
65					70					75					80
Ala	Arg	Thr	Glu	Lys	Ile	Gly	Asp	Gly	Lys	Ile	Phe	Val	Ser	Ser	Ile
				85					90					95	
Glu	Gln	Ala	Ile	Arg	Ile	Arg	Thr	Gly	Glu	Thr	Gly	Glu	Asp	Ala	Val

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Lys Lys Ile Glu Ala Ile Ile Arg Pro Phe Lys Leu Asp Glu Val
 1      5      10      15
Lys Ile Ala Leu Val Asn Ala Gly Ile Val Gly Met Thr Val Ser Glu
 20      25      30
Val Arg Gly Phe Gly Arg Gln Lys Gly Gln Thr Glu Arg Tyr Arg Gly
 35      40      45
Ser Glu Tyr Thr Val Glu Phe Leu Gln Lys Leu Lys Leu Glu Ile Val
 50      55      60
Val Glu Asp Ala Gln Val Asp Thr Val Ile Asp Lys Ile Val Ala Ala
 65      70      75      80
Ala Arg Thr Gly Glu Ile Gly Asp Gly Lys Ile Phe Val Ser Pro Val
 85      90      95
Asp Gln Thr Ile Arg Ile Arg Thr Gly Glu Lys Asn Ala Asp Ala Ile
100      105      110

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Lys Met Ile Lys Ala Ile Val Arg Pro Asp Lys Val Asp Asp Ile
 1      5      10      15
Val Asp Ser Leu Glu Asn Ala Gly Tyr Pro Ala Phe Thr Lys Ile Asn
 20      25      30
Ser Val Gly Arg Gly Lys Gln Gly Gly Leu Lys Val Gly Glu Ile Phe
 35      40      45
Tyr Asp Glu Leu Pro Lys Thr Ile Leu Leu Ile Ala Val Asn Asp Asp
 50      55      60
Glu Val Asp Glu Val Val Gly Leu Ile Lys Ser Ser Ala Ser Thr Gly
 65      70      75      80
Asn Phe Gly Asp Gly Lys Ile Phe Ile Gln Pro Ile Thr Glu Ala Tyr
 85      90      95
Thr Ile Arg Thr Gly Glu Thr Gly Ile
100      105

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Glu Val Ile Ala Ile Ile Arg Pro Asn Thr Val Ser Lys Thr
 1 5 10 15
 Val Lys Ala Leu Asp Val Val Gly Phe Pro Ala Val Thr Met Ala Glu
 20 25 30
 Cys Phe Gly Arg Gly Lys Gln Lys Gly Tyr Glu Glu Gly Glu Lys Glu
 35 40 45
 Gly Arg Phe Ile Lys Tyr Ile Pro Lys Arg Leu Ile Ser Ile Val Val
 50 55 60
 Asp Asp Ala Asp Val Pro Leu Val Val Gly Ile Ile Ser Lys Val Asn
 65 70 75 80
 Arg Thr Gly Ser Phe Gly Asp Gly Arg Ile Phe Val Leu Pro Val Glu
 85 90 95
 Glu Ala Ile Arg Val Arg Thr Gly Glu Thr Gly Glu Ile Ala Ile
 100 105 110

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Phe Ser Ala Asn Leu Pro Glu Ile Val Asp Ile Gln Lys Ile Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTGAAAGTTG	TGTTAAAAAA	AAAAC TAGAA	TCATGGCGGC	GTCAATGACG	AAACCCATCT	60
CAATAACTTC	TCTCGGTTTC	TATTCTGATC	GAAAGAACAT	TGCTTTCTCT	GATTGCATTT	120
CGATTTGTTC	TGGATTCAGA	CATTCCCGAC	CATCTTGCCCT	CGATTTGGTC	ACAAAGTCAC	180
CGAGTAATAA	CAGTCGTGTT	TTACCTGTCG	TTAGTGCCCA	AATATCTTCT	GATTATATTC	240
CAGACTCGAA	ATTTTACAAG	GTGGAAGCAA	TTGTCAGACC	ATGGAGAATC	CAGCAAGTTT	300
CATCGGCTTT	ACTGAAAATC	GGGATTCGAG	GTGTTACTGT	TTCTGATGTG	AGAGGGTTTG	360
GTGCACAAGG	AGGTTCTACC	GAGAGACACG	GTGGCTCTGA	GTTCTCGGAA	GACAAATTTG	420
TTGCTAAAGT	TAAGATGGAA	ATCGTTGTTA	AGAAAGACCA	AGTGAATCT	GTAATCAACA	480
CAATAATTGA	AGGAGCAAGG	ACAGGAGAGA	TTGGTGATGC	CAAGATTTTT	TTTTTGCCCTG	540
TGTCAGATGT	CATAAGAGTT	AGGACAGGTG	AGCGTGGGGA	GAAAGCAGAG	AAGATGACTG	600
GTGATATGCT	TTACCCGTCT	TAGGAACAAA	CAGAGCTCAA	GAATGGTTTT	TTTTTTTTTC	660
ATTTCCGTCT	CTAGATTCTG	CGAATAATAA	TGAATGGAGT	CTGTGTTTGG	TTTCATGTTG	720
AATCGATCAA	GATGTGTTTT	TAACTGTACA	TGAATTATGC	AGAAACATCT	GTCTGTGTTG	780
TCAGACATCG	AAACTCTGTT	CCTAATAAAA	AAAAAAA			817

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGTGTCGG	CCGCTCTAGA	ACTAGTGGAT	CCCCCGGGCT	GCAGGAATTC	GGCACGAGGC	60
TACTGCGAAA	CTGGGCTTGC	TCACTCCTCT	TCATTCTAAT	AACATCAAGA	AAGAATTCCC	120
TGTTTTTGAT	TTCAGTTTGT	TTTGTCAGAG	GCTTAGACAT	TCTCGGTTTT	CTCACTTTAA	180
CACCGCGGTC	AAGCGCGTAA	GATATGCCCC	CGTCGTTTCT	GTGATTAATG	CCCAAAGCTC	240
GCCTGACTAC	ATTCTTGATG	CTAAATTCTA	CAAAGTGGA	GCAATTCTCA	GGCCCTGGCG	300
AGTCTCGCAA	GTTCTCTCGG	CTTGCTAAA	AATTGGTATT	CGAGGTGTTA	CTGTTTCTGA	360
TGTTTCGAGG	TTTGGTGCTC	AAGGTGGTTC	AACTGAGAGG	CAGGGCGGCT	CAGAATTTTC	420
TGAAGACAAG	TTTGTTGCTA	AAGTTAAGAT	GGAGATCGTG	GTTAGCAAAG	ACCAGGTTGA	480
GGATGTTATA	GAAAAAATCA	TTGAGGAGGC	AAGAACTGGA	GAGATTGGAG	ACGGCAAGAT	540
TTTCTTGCTG	CCTGTTTCAG	ATGTAATAAG	AGTCCGCACT	GGTGAGCGGG	GTGATAAGGC	600
TGAGAGGATG	ACAGGAGGGC	GATCTGACAT	GAGTACTTCT	GCTTGACTGC	TGTGACCAGC	660
AATATAGCAT	TCAGGACTAA	CTGTCCTTTG	AGAAAGCCCC	GCCCTTATTA	GCCATTATCC	720
AGTATAGCTT	GATAATTTGA	ATTTTTTGTG	TTCTTAACTA	AAGAAACAAA	GATCTTTTCA	780
TTATCCTGTT	GATGATAATT	GAAAACGGAA	GGATCGCGAA	TTTGTTCAAG	TGCTTGCAAG	840
ATAAATAACA	AGAAGAGGAG	TAATGTTAAC	AAAAAAAAAA	AAAAAAAAAA	ACTCGAG	897

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGCGGCGT	CAATGACGAA	ACCCATCTCA	ATAACTTCTC	TCGGTTTCTA	TTCTGATCGA	60
AAGAACATTG	CTTTCTCTGA	TTGCATTTCT	ATTTGTTCTG	GATTCAGACA	TTCCCGACCA	120
TCTTGCCCTG	ATTTGGTCAC	AAAGTCACCG	AGTAATAACA	GTCGTGTTTT	ACCTGTCGTT	180
AGTGCCCAAA	TATCTTCTGA	TTATATTCCA	GACTCGAAAT	TTTACAAGGT	GGAAGCAATT	240
GTCAGACCAT	GGAGAATCCA	GCAAGTTTCA	TCGGCTTTAC	TGAAAATCGG	GATTCGAGGT	300
GTTACTGTTT	CTGATGTGAG	AGGGTTTGGT	GCACAAGGAG	GTTCTACCGA	GAGACACGGT	360
GGCTCTGAGT	TCTCGGAAGA	CAAATTTGTT	GCTAAAGTTA	AGATGGAAAT	CGTTGTTAAG	420
AAAGACCAAG	TGGAATCTGT	AATCAACACA	ATAATTGAAG	GAGCAAGGAC	AGGAGAGATT	480
GGTGATGGCA	AGATTTTGTG	TTTGCCCTGT	TCAGATGTCA	TAAGAGTTAG	GACAGGTGAG	540
CGTGCGGAGA	AAGCAGAGAA	GATGACTGGT	GATATGCTTT	CACCGTCT		588

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGCACGAGG	CTACTGCGAA	ACTGGGCTTG	CTCACTCCTC	TTCATTCTAA	TAACATCAAG	60
AAAGAATTCC	CTGTTTTTGA	TTTCAGTTTG	TTTTGTCCAG	AGCTTAGACA	TTCTCGGTTT	120
TCTCACTTTA	ACACCGCGGT	CAAGCGCGTA	AGATATGCCC	CCGTCGTTCC	TGTGATTAAT	180
GCCCAAAGCT	CGCCTGACTA	CATTCCTGAT	GCTAAATTCT	ACAAAGTGGA	AGCAATTCTC	240
AGGCCCTGGC	GAGTCTCGCA	AGTTTCCTCG	GCTTTGCTAA	AAATTGGTAT	TCGAGGTGTT	300
ACTGTTTCTG	ATGTTTCGAG	TTTTGGTGCT	CAAGGTGGTT	CAACTGAGAG	GCAGGGCGGC	360
TCAGAATTTT	CTGAAGACAA	GTTTGTTGCT	AAAGTTAAGA	TGGAGATCGT	GGTTAGCAAA	420
GACCAGGTTG	AGGATGTTAT	AGAAAAAATC	ATTGAGGAGG	CAAGAAGTGG	AGAGATTGGA	480
GACGGCAAGA	TTTTCTTGCT	GCCTGTTTCA	GATGTAATAA	GAGTCCGCAC	TGGTGAGCGG	540
GGTGATAAGG	CTGAGAGGAT	GACAGGAGGG	CGATCTGACA	TGAGTACTTC	TGCT	594

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAAGATGGT CGGGAATGTC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGACAGGTAA AACACGACTG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGACAA TTGCTTCCAC

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAAACCAAAC ACAGACTCC

19

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGAGTAATA ACAGTCGTC

19